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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/035,060C

DATE: 03/13/2003

TIME: 14:19:22

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF4\03132003\J035060C.raw

3 <110> APPLICANT: Edwards, David L.
 4 Hernstadt, Corinna
 5 Wilcox, Edward R.
 6 Wong, Siu-Yin
 8 <120> TITLE OF INVENTION: Process for Altering the Host Range of *Bacillus*
thuringiensis Toxins, and
 9 Novel Toxins Produced Thereby
 11 <130> FILE REFERENCE: M12C1FDF3D2
 13 <140> CURRENT APPLICATION NUMBER: US 10/035,060C
 14 <141> CURRENT FILING DATE: 2001-12-27
 16 <150> PRIOR APPLICATION NUMBER: US 09/405,788
 17 <151> PRIOR FILING DATE: 1999-09-27
 19 <150> PRIOR APPLICATION NUMBER: US 08/855,160
 20 <151> PRIOR FILING DATE: 1997-05-13
 22 <150> PRIOR APPLICATION NUMBER: US 08/580,781
 23 <151> PRIOR FILING DATE: 1995-12-29
 25 <150> PRIOR APPLICATION NUMBER: US 08/420,615
 26 <151> PRIOR FILING DATE: 1995-04-10
 28 <150> PRIOR APPLICATION NUMBER: US 08/097,808
 29 <151> PRIOR FILING DATE: 1993-07-27
 31 <150> PRIOR APPLICATION NUMBER: US 07/980,128
 32 <151> PRIOR FILING DATE: 1992-11-23
 34 <150> PRIOR APPLICATION NUMBER: US 07/803,920
 35 <151> PRIOR FILING DATE: 1991-12-06
 37 <150> PRIOR APPLICATION NUMBER: US 07/356,599
 38 <151> PRIOR FILING DATE: 1989-05-24
 40 <150> PRIOR APPLICATION NUMBER: US 06/904,572
 41 <151> PRIOR FILING DATE: 1986-09-05
 43 <150> PRIOR APPLICATION NUMBER: US 06/808,129
 44 <151> PRIOR FILING DATE: 1985-12-12
 46 <160> NUMBER OF SEQ ID NOS: 9
 48 <170> SOFTWARE: PatentIn version 3.1
 50 <210> SEQ ID NO: 1
 51 <211> LENGTH: 3531
 52 <212> TYPE: DNA
 53 <213> ORGANISM: *Bacillus thuringiensis*
 55 <400> SEQUENCE: 1
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 58 gtagaagtat taggtggaga aagaatagaa actggttaca cccaatcga tatttccttg 120
 60 tcgctaacgc aatttccttt gagtgaattt gttcccgggtg ctggatttgt gttaggacta 180
 62 gttgatataa tatggggaat ttttgggtccc tctcaatggg acgcatttct tgtacaaatt 240
 64 gaacagttaa ttaaccaaag aatagaagaa ttcgctagga accaagccat ttctagatta 300
 66 gaaggactaa gcaatcttta tcaaatttac gcagaatctt ttagagagtg ggaagcagat 360
 68 cctactaatc cagcattaag agaagagatg cgtattcaat tcaatgacat gaacagtgcc 420

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76	ggcaactata	cagattatgc	tgtacgctgg	tacaatacgg	gattagaacg	tgtatgggga	660
78	ccggattcta	gagattgggt	aaggtataat	caatttagaa	gagaattaac	actaactgta	720
80	ttagatatac	ttgctctgtt	cccgaattat	gatagtagaa	gatatccaat	tcgaacagtt	780
82	tcccaattaa	caagagaaat	ttatacaaac	ccagtattag	aaaattttga	tggtagtttt	840
84	cgaggctcgg	ctcagggcac	agaaagaagt	attaggagtc	cacatttgat	ggatatactt	900
86	aacagtataa	ccatctatac	ggatgctcat	aggggttatt	attattggtc	agggcatcaa	960
88	ataatggctt	ctcctgtagg	gttttcgggg	ccagaattca	cttttccgct	atatggaact	1020
90	atgggaaatg	cagctccaca	acaacgtatt	gttgctcaac	taggtcaggg	cgtgtataga	1080
92	acattatcgt	ccactttata	tagaagacct	tttaatatag	ggataaataa	tcaacaacta	1140
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96	tacagaaaaa	gcggaacggt	agattcgctg	gatgaaatac	cgccacagaa	taacaacgtg	1260
98	ccacctaggc	aaggatttag	tcatcgatta	agccatgttt	caatgtttcg	ttcaggcttt	1320
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156	caaaacaacc	aacgttcggg	ccttgttctt	ccggaatggg	aagcagaagt	gtcacaagaa	3060
158	gttcgtgtct	gtccgggtcg	tggctatata	cttcgtgtca	cagcgtacaa	ggagggatat	3120
160	ggagaagggt	gcgtaaccat	tcagtagatc	gagaacaata	cagacgaact	ggagtttagc	3180
162	aactgcgtag	aagaggaaat	ctatccaaat	aacacggtaa	cgtgtaatga	ttatactgta	3240
164	aatcaagaag	aatacggagg	tgcgtacact	tctcgtaatc	gaggatataa	cgaagctcct	3300
166	tccgtaccag	ctgattatgc	gtcagttcat	gaagaaaaat	cgtatacaga	tgagacgaaga	3360

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168 gagaatcctt gtgaatttaa cagagggtat agggattaca cgccactacc agttgggttat 3420
170 gtgacaaaag aattagaata cttcccagaa accgataagg tatggattga gattggagaa 3480
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175 <210> SEQ ID NO: 2
176 <211> LENGTH: 1177
177 <212> TYPE: PRT
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180 <400> SEQUENCE: 2
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183 1 5 10 15
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187 20 25 30
190 Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
191 35 40 45
194 Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
195 50 55 60
198 Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
199 65 70 75 80
202 Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
203 85 90 95
206 Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
207 100 105 110
210 Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
211 115 120 125
214 Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
215 130 135 140
218 Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
219 145 150 155 160
222 Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
223 165 170 175
226 Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
227 180 185 190
230 Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
231 195 200 205
234 Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
235 210 215 220
238 Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
239 225 230 235 240
242 Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
243 245 250 255
246 Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
247 260 265 270
250 Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
251 275 280 285
254 Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
255 290 295 300
258 Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Tyr Trp Ser Gly His Gln
259 305 310 315 320
262 Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro

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266 Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
267          340          345          350
270 Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
271          355          360          365
274 Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
275          370          375          380
278 Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
279 385          390          395          400
282 Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
283          405          410          415
286 Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
287          420          425          430
290 Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
291          435          440          445
294 Arg Ala Pro Thr Phe Ser Trp Gln His Arg Ser Ala Glu Phe Asn Asn
295          450          455          460
298 Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr
299 465          470          475          480
302 Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly
303          485          490          495
306 Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg
307          500          505          510
310 Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg
311          515          520          525
314 Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg
315          530          535          540
318 Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn
319 545          550          555          560
322 Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn
323          565          570          575
326 Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn
327          580          585          590
330 Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu
331          595          600          605
334 Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val
335          610          615          620
338 Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val
339 625          630          635          640
342 Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser
343          645          650          655
346 Asp Glu Phe Cys Leu Asp Glu Lys Gln Glu Leu Ser Glu Lys Val Lys
347          660          665          670
350 His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn
351          675          680          685
354 Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr
355          690          695          700
358 Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val
359 705          710          715          720

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362 Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
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366 Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
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370 Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
371              755              760              765
374 Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp
375              770              775              780
378 Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg
379 785              790              795              800
382 Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg
383              805              810              815
386 Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile
387              820              825              830
390 Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile
391              835              840              845
394 Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu
395              850              855              860
398 Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys
399 865              870              875              880
402 Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu
403              885              890              895
406 Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe
407              900              905              910
410 Val Asn Ser Gln Tyr Asp Gln Leu Gln Ala Asp Thr Asn Ile Ala Met
411              915              920              925
414 Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu
415              930              935              940
418 Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu
419 945              950              955              960
422 Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn
423              965              970              975
426 Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val
427              980              985              990
430 Lys Gly His Val Asp Val Glu Glu Gln Asn Asn Gln Arg Ser Val Leu
431              995              1000              1005
434 Val Leu Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val
435              1010              1015              1020
438 Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu
439              1025              1030              1035
442 Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn
443              1040              1045              1050
446 Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Ile Tyr
447              1055              1060              1065
450 Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Val Asn Gln Glu
451              1070              1075              1080
454 Glu Tyr Gly Gly Ala Tyr Thr Ser Arg Asn Arg Gly Tyr Asn Glu
455              1085              1090              1095
458 Ala Pro Ser Val Pro Ala Asp Tyr Ala Ser Val Tyr Glu Glu Lys

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